

3.5

Eco RI

Kpn I (158)

Pst I (538)

Sac I (661)

Pvu II (715)

Pvu II (836)

Pvu II (1046)

Pst I (1156)

Sma I (1309)

Pvu II (1429)

Sma I (1595)

Pvu II (1880)

Bam HI (2101)

Sma I (2417)

Pvu II (2771)

Bgl II (2872)

Eco RI



FIG. 1B-1

1 GCCATCTGGGCCCAAGGCCCATGCCCGGAGGGGTGGTCTGAAGGCCCAACCCAGAGCCCCCTGCCAGACTGTCTGCCTCCCTTCTGACTC

21

11

MetAlaSerAsnSerSerCysProThrProGlyGlyGlyHisLeuAsnGlyTyrProValProProTyrAlaPhe

91 TGGCGCTTGGCATGGCCAGCAACAGCAGCTCTGCCGACACCTGGGGCGGGCACCTCAATGGGTACCCGGTGCCTCCCTACGGCTTC

31

41

51

PhePheProMetLeuGlyGlyLeuSerProProGlyAlaLeuThrThrLeuGlnHisGlnLeuProValSerGlyTyrSerThrPro

181 TTCTTCCCCCTATGCTGGGTGGACTCTCCCCGCCAGGCGCTCTGACCACTCTCCAGCACCACTTCCAGTTAGTGGATATAGCACACCA

61

71

81

SerProAlaThrIleGluThrGlnSerSerSerSerSerGluGluIleValProSerProProSerProProLeuProArgIleTyrLys

271 TCCCCAGGCACCATTTGAGACCCAGAGCAGATTCTGAAGAGATAGTGGCAGGCCCTCCCTCGCCACCCCTCTACCCCGCATCTACAAG

FIG. 1B-2

91 101 111
ProCysPheValCysGlnAspLysSerGlyTyrHisTyrGlyValSerAlaCysGluGlyCysLysGlyPhePheArgSerIle
361 CCTTGGCTTTGTCTGTCTCAGGCAAGTCTCTAGGCTACCACTATGGGTGAGGGCTGCAAGGGCTTCTTCGGCCGCGAGCATC
121 131 141
GlnLysAsnMetValTyrThrCysHisArgAspLysAsnCysIleIleAsnLysValThrArgAsnArgCysGlnTyrCysArgLeuGln
451 CAGAAGAACAATGGTGTACAGTGTACCGGGACAAGAACTGCATCATCAACAAGGTGACCCGGAACCGCTGCCAGTACTGCCGACTGCAG
151 161 171
LysCysPheGluValGlyMetSerLysGluSerValArgAsnAspArgAsnLysLysLysGluValProLysProGluCysSerGlu
541 AAGTGTCTTGAAGTGGCATGTCCAAAGGAGTCTGTGAGAAACGACCGAAACGAAGAAGAGGAGGTGCCCAAGCCGAGTGTCTCTGAG
181 191 201
SerTyrThrLeuThrProGluValGlyGluLeuIleGluLysValArgLysAlaHisGlnGluThrPheProAlaLeuCysGlnLeuGly
631 AGCTACAGCTGACGCCGAGGTGGGGAGCTCATTGAGAAGGTGGCGAAAGCGCACCAAGAAACCTTCCCTGCCCTCTGCCAGCTGGGC
211 221 231
LysTyrThrThrAsnAsnSerSerGluGlnArgValSerLeuAspIleAspLeuTrpAspLysPheSerGluLeuSerThrLysCysIle
721 AAATACACTACGAACAACAGCTCAGAACACCGTGTCTCTGTGACATTGACCTCTGGGACAAGTTCAAGTGAACCTCTCCACCAAGTGCATC
241 251 261
IleLysThrValGluPheAlaLysGlnLeuProGlyPheThrThrLeuThrIleAlaAspGlnIleThrLeuLeuLysAlaAlaCysLeu
811 ATTAAGACTGTGGAGTTGCCCAAGCAGCTGCCCGGCTTCACCACTCACCCTCAGCTCGCCGACCAAGATCACCTCTCAAGGCTGCCTGCCTG
271 281 291
AspIleLeuIleLeuArgIleCysThrArgTyrThrProGluGlnAspThrMetThrPheSerAspGlyLeuThrLeuAsnArgThrGln
901 GACATCCTGATCCTGCGGATCTGCACGCGGTACACGCCGAGCAGGACACCATGACCTTCTCGGACGGGCTGACCCCTGAACCGGACCCAG
301 311 321
MetHisAsnAlaGlyPheGlyProLeuThrAspLeuValPheAlaPheAlaAsnGlnLeuLeuProLeuMetAspAspAlaGluThr
991 ATGCACAACGCTGGCTTCGGCCCCCTCACCGACCTGGTCTTTGCCCTTCGCCAACCAAGCTGCTGCCCTGGAGATGGATGCGGAGACG
331 341 351
GlyLeuLeuSerAlaIleCysLeuIleCysGlyAspArgGlnAspLeuGlnProAspArgValAspMetLeuGlnGluProLeuLeu
1081 GGGCTGCTCAGCGCCATCTGCCTCATCTGCGGAGACCGCGGAGACCTGGAGCAGCGCGGCTGGACATGCTGCAGGAGCCGCTGCTG

FIG. 1B-3

11171	361	371	381	391	401	411	421	431	441	451	461	471	481	491	501	511	521	531	541	551	561	571	581	591	601	611	621	631	641	651	661	671	681	691	701	711	721	731	741	751	761	771	781	791	801	811	821	831	841	851	861	871	881	891	901	911	921	931	941	951	961	971	981	991	1001	1011	1021	1031	1041	1051	1061	1071	1081	1091	1101	1111	1121	1131	1141	1151	1161	1171	1181	1191	1201	1211	1221	1231	1241	1251	1261	1271	1281	1291	1301	1311	1321	1331	1341	1351	1361	1371	1381	1391	1401	1411	1421	1431	1441	1451	1461	1471	1481	1491	1501	1511	1521	1531	1541	1551	1561	1571	1581	1591	1601	1611	1621	1631	1641	1651	1661	1671	1681	1691	1701	1711	1721	1731	1741	1751	1761	1771	1781	1791	1801	1811	1821	1831	1841	1851	1861	1871	1881	1891	1901	1911	1921	1931	1941	1951	1961	1971	1981	1991	2001	2011	2021	2031	2041	2051	2061	2071	2081	2091	2101	2111	2121	2131	2141	2151	2161	2171	2181	2191	2201	2211	2221	2231	2241	2251	2261	2271	2281	2291	2301	2311	2321	2331	2341	2351	2361	2371	2381	2391	2401	2411	2421	2431	2441	2451	2461	2471	2481	2491	2501	2511	2521	2531	2541	2551	2561	2571	2581	2591	2601	2611	2621	2631	2641	2651	2661	2671	2681	2691	2701	2711	2721	2731	2741	2751	2761	2771	2781	2791	2801	2811	2821	2831	2841	2851	2861	2871	2881	2891	2901	2911	2921	2931	2941	2951	2961	2971	2981	2991	3001	3011	3021	3031	3041	3051	3061	3071	3081	3091	3101	3111	3121	3131	3141	3151	3161	3171	3181	3191	3201	3211	3221	3231	3241	3251	3261	3271	3281	3291	3301	3311	3321	3331	3341	3351	3361	3371	3381	3391	3401	3411	3421	3431	3441	3451	3461	3471	3481	3491	3501	3511	3521	3531	3541	3551	3561	3571	3581	3591	3601	3611	3621	3631	3641	3651	3661	3671	3681	3691	3701	3711	3721	3731	3741	3751	3761	3771	3781	3791	3801	3811	3821	3831	3841	3851	3861	3871	3881	3891	3901	3911	3921	3931	3941	3951	3961	3971	3981	3991	4001	4011	4021	4031	4041	4051	4061	4071	4081	4091	4101	4111	4121	4131	4141	4151	4161	4171	4181	4191	4201	4211	4221	4231	4241	4251	4261	4271	4281	4291	4301	4311	4321	4331	4341	4351	4361	4371	4381	4391	4401	4411	4421	4431	4441	4451	4461	4471	4481	4491	4501	4511	4521	4531	4541	4551	4561	4571	4581	4591	4601	4611	4621	4631	4641	4651	4661	4671	4681	4691	4701	4711	4721	4731	4741	4751	4761	4771	4781	4791	4801	4811	4821	4831	4841	4851	4861	4871	4881	4891	4901	4911	4921	4931	4941	4951
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FIG. 2A

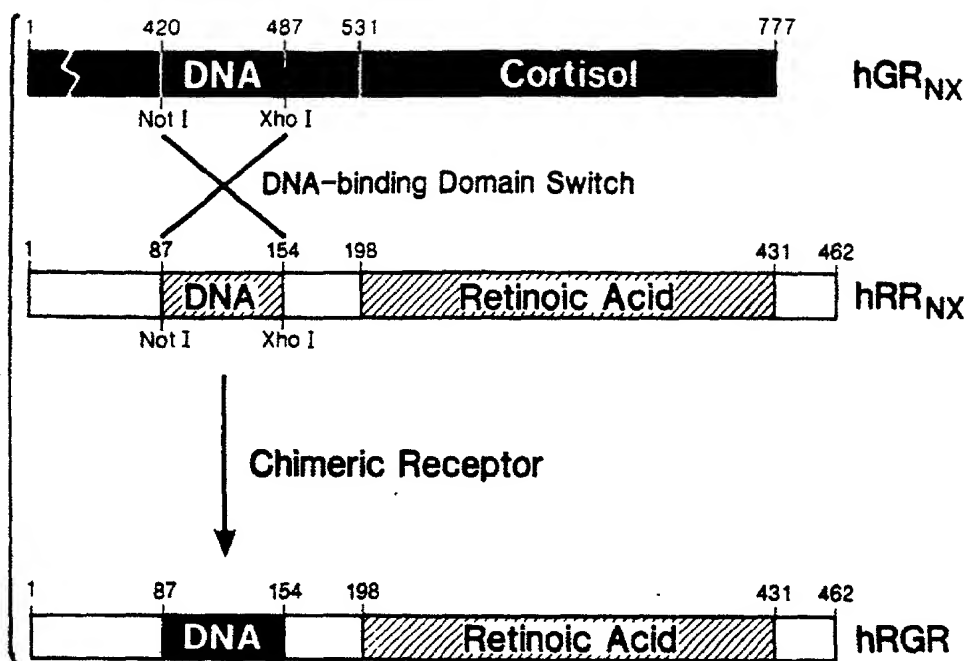


FIG. 2B

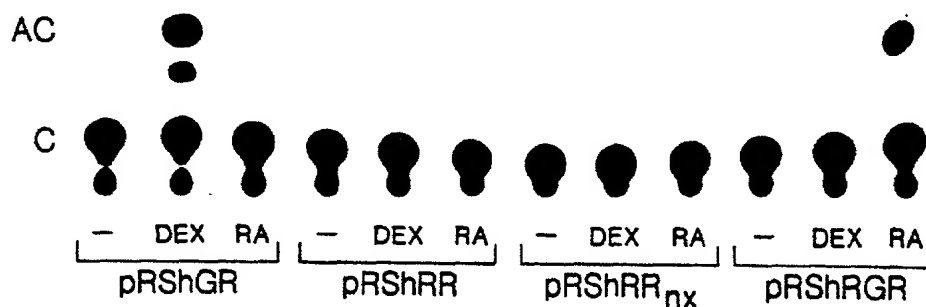


FIG. 3A

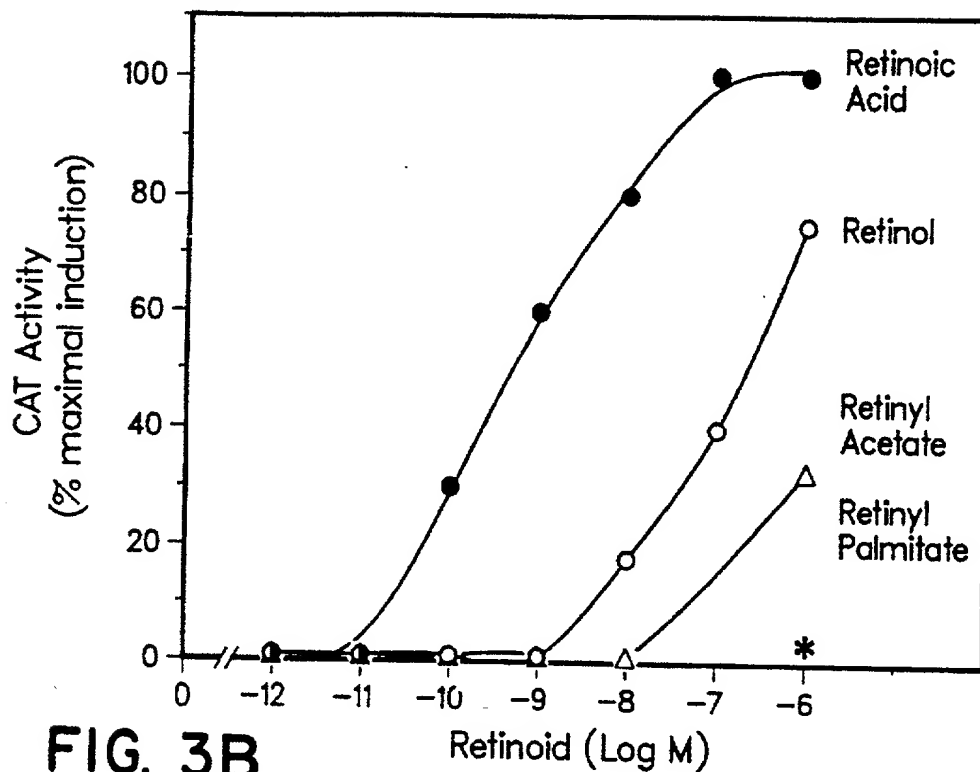


FIG. 3B

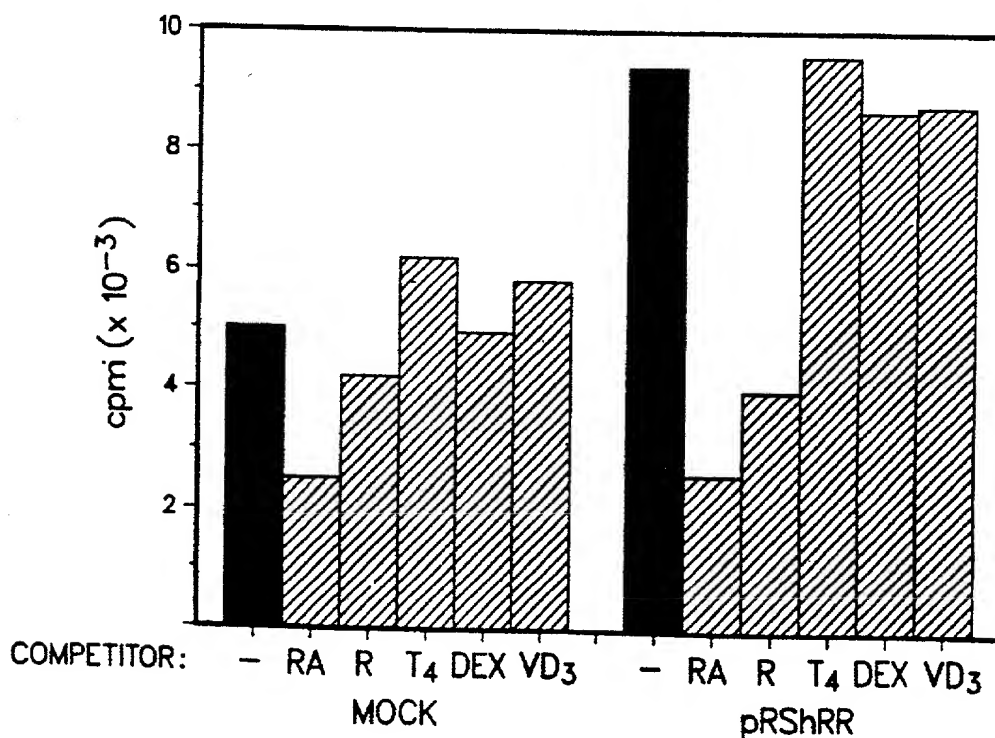


FIG. 4A

Bam HI
Bgl II
EcoRI
Hind III
Pst I
Pvu II

23.0-

9.5-

6.6-

4.2-

2.3-

2.0-

0.5-

FIG. 4B

Bam HI
Bgl II
EcoRI
Hind III
Pst I
Pvu II

FIG. 4A

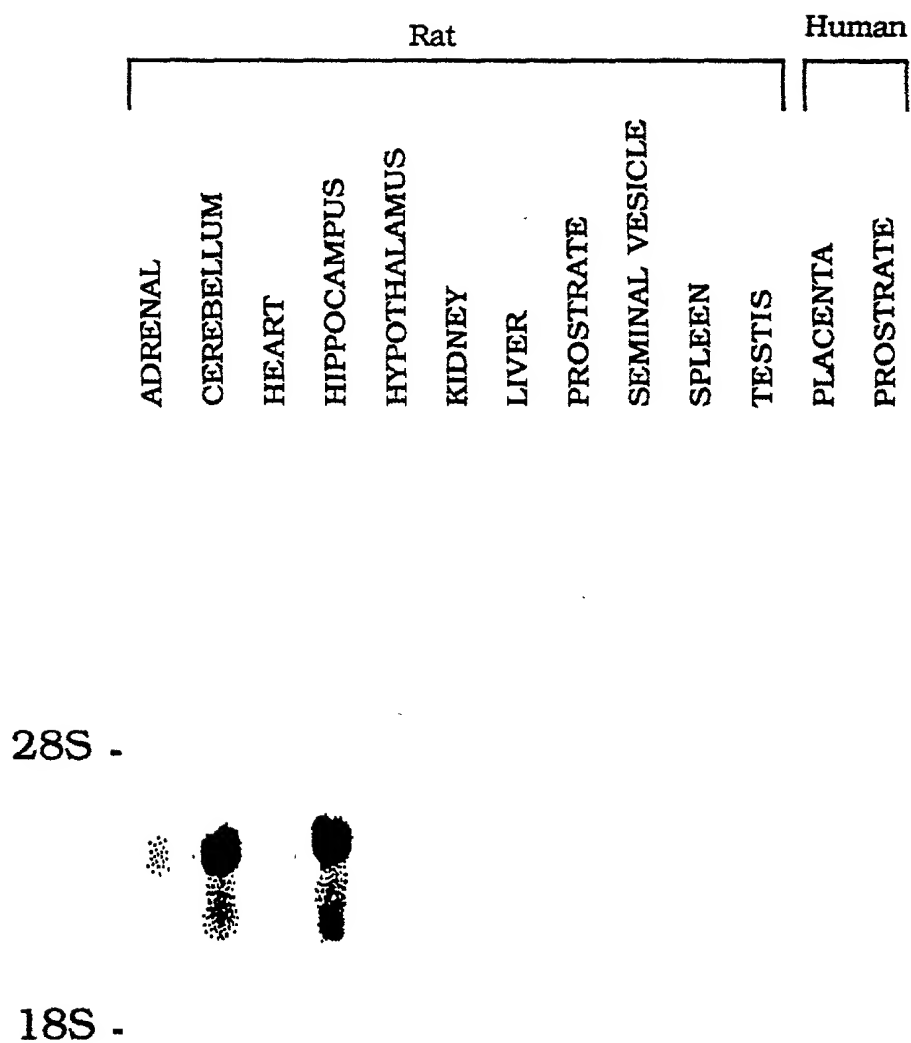


FIGURE 5

FIG. 6

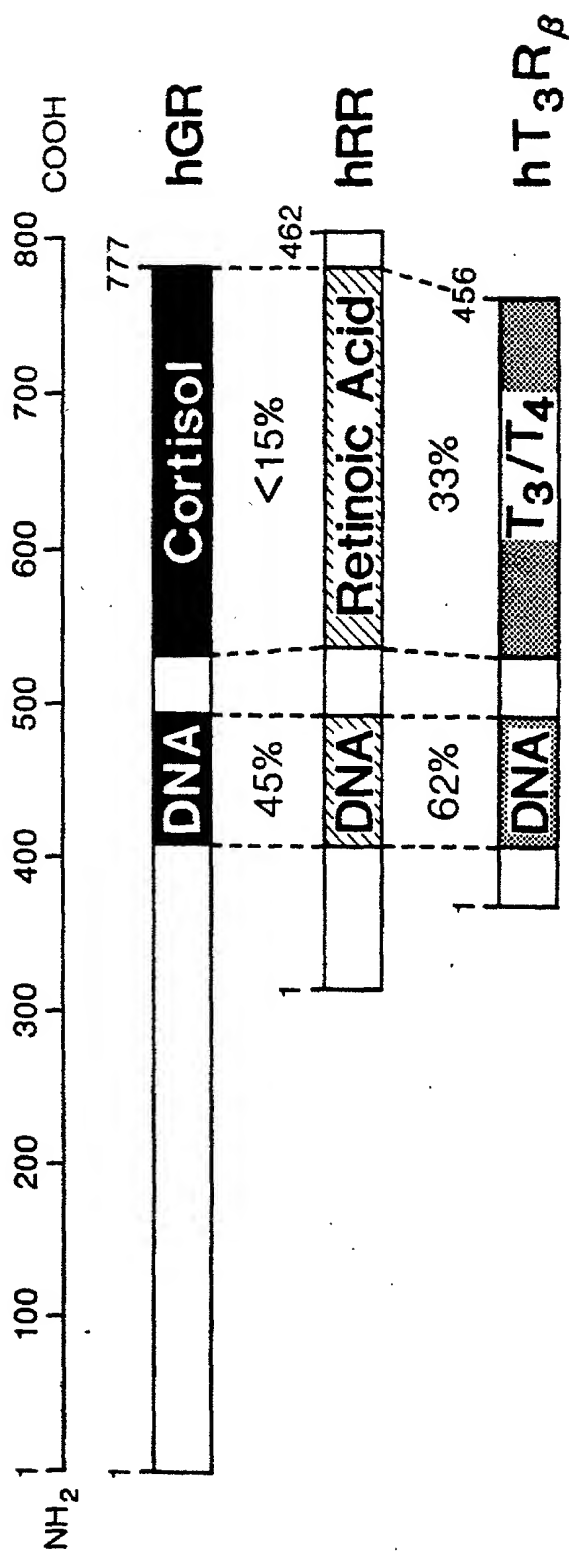


FIG. 7

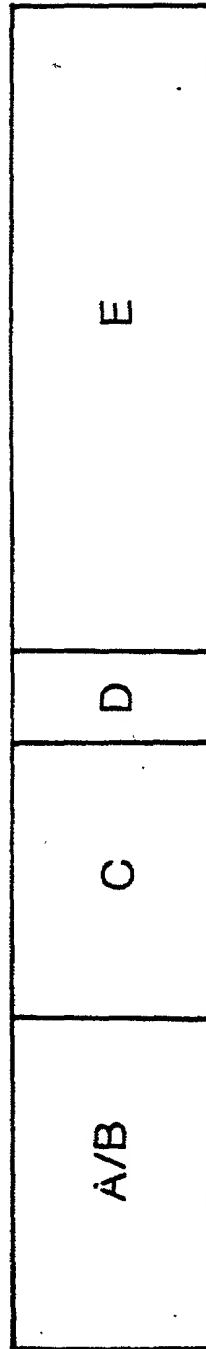


FIG. 8-1

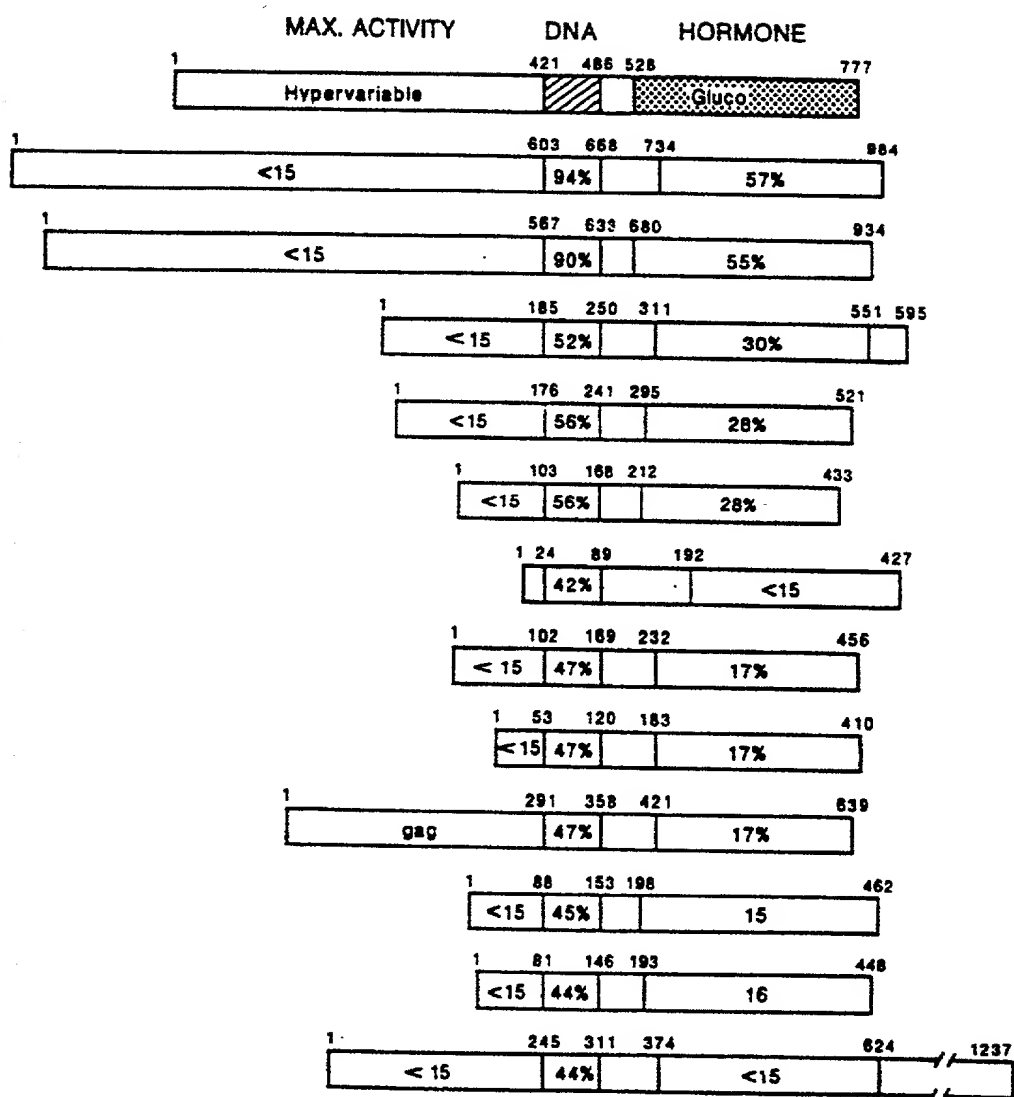


FIG. 8-2

	HRE	DNA BINDING	HORMONE BINDING		TRANS- ACTIVATION	CHROMO- SOME	SPECIES
			IN VITRO	IN VIVO			
GR	+ ¹⁵⁻¹⁹	+ ^{16,17,21}	+ ^{25,82}	+ ^{48,52, 77}	+ ^{48,52, 78,79}	5 ²⁶	h, ²⁶ r, ⁷⁷ m, ⁷⁸
MR	nd	nd	nd	+ ³⁶	+ ³⁶	4 ³⁶	h ³⁶
PR	+ ^{24,34}	+ ^{24,34}	nd	nd	+ ³⁴	11 ⁷⁹	rabbit, ³² h, ³³ c, ³⁴
ER	+ ^{22,23}	+ ^{23,62}	nd	+ ^{23,53, 62}	+ ^{53,62}	6 ⁶²	h, ²⁹ c, ³⁰ frog ³¹
ERR1	nd	nd	nd	nd	nd	nd	h ³⁹
ERR2	nd	nd	nd	nd	nd	nd	h ³⁹
VDR	nd	nd	nd	+ ³⁵	nd	nd	h, ³⁵ c ³⁵
T ₃ R _β	+ ²⁵	+ ²⁵	+ ³⁷	nd	+ ⁸⁰	3 ³⁷	h ³⁷
T ₃ R _α	nd	nd	+ ^{38,40}	nd	+ ⁸⁰	17 ⁴⁰	r, ⁴⁰ h, ⁴¹ c ³⁸
V-erb A	+	+	(-) ³⁸	nd	nd	virus	c ²⁸
RAR	nd	nd	nd	+ ^{42,43}	+ ^{42,43}	17 ⁸³	h ^{42,43}
HAP	nd	nd	nd	nd	nd	3 ⁴⁵	h ⁴⁵
E75	nd	nd	nd	nd	nd		d ⁴⁶

FIG. 9

The diagram illustrates the structure of DNA constructs for TRE and GRE reporter systems. The constructs are organized into two main groups: TRE-1MCA and GRE-1MCA. Each group contains five constructs, labeled AAB. The constructs are represented by horizontal bars divided into segments. The segments are labeled with DNA elements: NotI, XbaI, DNA, T3/T4, TTT(hTRβnX), ΔTT, TTG, GTT, GTG, GGG(hGRnX), GGT, TGG, TGT, and ΔGG. The hormone treatment for each construct is indicated by a label above the bar: T3, T3, dex, T3, dex for TRE-1MCA; and dex, T3, dex, T3, dex for GRE-1MCA. The hormone treatments are indicated by a label above the bar: T3, T3, dex, T3, dex for TRE-1MCA; and dex, T3, dex, T3, dex for GRE-1MCA. The hormone treatments are indicated by a label above the bar: T3, T3, dex, T3, dex for TRE-1MCA; and dex, T3, dex, T3, dex for GRE-1MCA.

AAB = Activation Above Background